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APPENDIX A

AF106851
LOCUS AF106851 2816 bp DNA linear BCT 08-APR-1999
DEFINITION Staphylococcus aureus LytN (lytN) and FmhC (fmhC) genes, complete cds.
ACCESSION AF106851
VERSION AF106851.1 GI:4574236
KEYWORDS .
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2816)
AUTHORS Tschierske, M., Mori, C., Rohrer, S., Ehlert, K., Shaw, K.J. and Berger-Bachi, B.
TITLE Identification of three additional femAB-like open reading frames in Staphylococcus aureus
JOURNAL FEMS Microbiol. Lett. 171 (2), 97-102 (1999)
MEDLINE 99177558
PUBMED 10077832
REFERENCE 2 (bases 1 to 2816)
AUTHORS Shaw, K.J.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-1998) Chemotherapy and Molecular Genetics, Schering-Plough Research Institute, 2015 Galloping Hill Road 4700, Kenilworth, NJ 07033, USA
FEATURES
source Location/Qualifiers
1. .2816
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/db_xref="ATCC:55748"
/db_xref="taxon:1280"
gene 193. .1344
/gene="lytN"
CDS 193. .1344
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/note="autolysin homolog"
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/translation="MFIYYCKECSIMNKQQSKVRYRSIRKVSIGILSISIGMFLALGMS
NKAYADEIDKSKDFTRGYEQNVFAKSELNANKNTTKDKIKNEGAVKTSDTSLKLDNKS
AISNGNEINQDIKISNTPKNSSQGNNLVINNNEPTKEIKIANLEAQNSNQKKTNKVTN
NYFGYYSFREAPKTQIYTVKKGDTLSAIALKYKTTVSNIQNTNNIANPNLIFIGQKLK
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/db_xref="GI:4574238"
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FILVDPYLIENLRDANGRIIKNYNNSVIVKMLGKIGYLHQGYTTGYSNKSQIRWISVL
DLKDKDENQLLKEMEYQTRRNKKTIEIGVKVEDLSIEETNRFYKLFQMAEEKHGFHF
MNEDYFKRMQEIYKDKAMLKIAICINLNEYQDKLKIQLKIEENMMTVNRALNENPNSK

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RNKS KLNQLNMQLSSINNRI SKTEELILEDGPVLDLAAALFICTDDEVYLLSSGSNPK
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IGDFIKPVRPILYKFAKLIYKV"

ORIGIN

Alignment Scores:

Pred. No.:	1.1e-147	Length:	2816
Score:	2176.00	Matches:	414
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-932-474-1 (1-414) x AF106851 (1-2816)

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Qy	21	HisTyrThrGlnSerIleGluLeuTyrAsnTyrArgAsnLysIleAsnHisGluAlaHis	40
Db	1432	CATTATACACAGTCTATAGAATTATATAATTATAGAAATAAAATAAATCATGAAGCACAT	1491
Qy	41	IleValGlyValLysAsnAspLysAsnGluValIleAlaAlaCysLeuLeuThrGluAla	60
Db	1492	ATTGTGGGAGTGAAGAATGATAAAAATGAAGTTATAGCTGCATGTTTATTAACAGAGGCA	1551
Qy	61	ArgIlePheLysPheTyrLysTyrPheTyrSerHisArgGlyProLeuLeuAspTyrPhe	80
Db	1552	CGAATTTTAAATTTACAAATATTTCTACTCTCATAGAGGTCCTTTACTTGATTATTTC	1611
Qy	81	AspAlaLysLeuValCysTyrPhePheLysGluLeuSerLysPheIleTyrLysAsnArg	100
Db	1612	GATGTCAAATAGTTTGTACTTTTAAAGAATTATCTAAATTCATTATAAAAATAGA	1671
Qy	101	GlyValPheIleLeuValAspProTyrLeuIleGluAsnLeuArgAspAlaAsnGlyArg	120
Db	1672	GGAGTATTTATTCTTGTGTGATCCATATTTAATAGAGAATTTAAGAGATGCAATGGTAGG	1731
Qy	121	IleIleLysAsnTyrAsnAsnSerValIleValLysMetLeuGlyLysIleGlyTyrLeu	140
Db	1732	ATAATAAAGAAATTATAATAATTCAGTGATAGTAAAGATGCTAGGGAAAATTGGGTATCTC	1791
Qy	141	HisGlnGlyTyrThrThrGlyTyrSerAsnLysSerGlnIleArgTrpIleSerValLeu	160
Db	1792	CATCAAGGTTATACAACAGGATATTCAAATAAAAGTCAAATTAGGTGGATTCTGTATTG	1851
Qy	161	AspLeuLysAspLysAspGluAsnGlnLeuLeuLysGluMetGluTyrGlnThrArgArg	180
Db	1852	GATTTAAAAGATAAAGATGAGAATCAACTTTTAAAAGAAATGGAATACCAACTAGAAGA	1911
Qy	181	AsnIleLysLysThrIleGluIleGlyValLysValGluAspLeuSerIleGluGluThr	200
Db	1912	AATATAAAAAGACTATTGAGATTGGTGTAAAGTTGAAGATTATCTATTGAAGAAACA	1971
Qy	201	AsnArgPheTyrLysLeuPheGlnMetAlaGluGluLysHisGlyPheHisPheMetAsn	220
Db	1972	AATCGATTTTATAAATTGTTTCAATGGCTGAAGAAAACATGGTTTTCATTTCATGAAT	2031
Qy	221	GluAspTyrPheLysArgMetGlnGluIleTyrLysAspLysAlaMetLeuLysIleAla	240
Db	2032	GAAGATTATTTTAAACGAATGCAAGAAATATATAAAGATAAGGCAATGTAAAGATAGCT	2091
Qy	241	CysIleAsnLeuAsnGluTyrGlnAspLysLeuLysIleGlnLeuLeuLysIleGluAsn	260
Db	2092	TGTATAAATCTTAATGAATATCAAGATAAATTAATAACAATTATTGAAAATCGAAAAT	2151

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Qy	261	GluMetMetThrValAsnArgAlaLeuAsnGluAsnProAsnSerLysArgAsnLysSer	280
Db	2152	GAAATGATGACTGTGAACAGAGCATTAAATGAAAATCCAAATCTCTAAAAGGAATAAATCA	2211
Qy	281	LysLeuAsnGlnLeuAsnMetGlnLeuSerSerIleAsnAsnArgIleSerLysThrGlu	300
Db	2212	AAATTTAAATCAGTTAAATATGCAATTATCTAGTATTAAATAATAGAATTAGTAAAACCAGAA	2271
Qy	301	GluLeuIleLeuGluAspGlyProValLeuAspLeuAlaAlaAlaLeuPheIleCysThr	320
Db	2272	GACTAATATTAGAAGATGGACCTGTTTTGGATTTAGCTGCTGCTTTATTTATATGTACT	2331
Qy	321	AspAspGluValTyrTyrLeuSerSerGlySerAsnProLysTyrAsnGlnTyrMetGly	340
Db	2332	GATGATGAAGTTTATTATCTATCAAGTGATCAAATCCGAAATATAATCAGTATATGGGT	2391
Qy	341	AlaTyrHisLeuGlnTrpHisMetIleLysTyrAlaLysSerHisAsnIleAsnArgTyr	360
Db	2392	GCATATCATCTACAATGGCATATGATAAAATATGCAAATCACATAATATTAATAGGTAT	2451
Qy	361	AsnPheTyrGlyIleThrGlyValPheSerAsnGluAlaAspAspPheGlyValGlnGln	380
Db	2452	AATTTTTATGGAATAACAGGCGTCTTTAGTAATGAGGCGGATGATTTTGGTGTTCAACAA	2511
Qy	381	PheLysLysGlyPheAsnAlaHisValGluGluLeuIleGlyAspPheIleLysProVal	400
Db	2512	TTTAAAAAGGGTTTTAATGCACATGTTGAAGAATTAATTGGTGATTTTCATCAAACCAGTA	2571
Qy	401	ArgProIleLeuTyrLysPheAlaLysLeuIleTyrLysVal	414
Db	2572	AGACCAATTCTATATAAAATTTGCAAAACTTATTTATAGGTT	2613

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APPENDIX B

Q9S685

ID Q9S685 PRELIMINARY; PRT; 414 AA.
AC Q9S685;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FmhC.
GN FMHC.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC55748;
RX MEDLINE=99177558; PubMed=10077832;
RA Tschierske M., Mori C., Rohrer S., Ehlert K., Shaw K.J.,
RA Berger-Bachi B.;
RT "Identification of three additional femAB-like open reading frames in
RT Staphylococcus aureus.";
RL FEMS Microbiol. Lett. 171:97-102(1999).
DR EMBL; AF106851; AAD23963.1; -.
DR GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.
DR InterPro; IPR003447; Meth_resist.
DR Pfam; PF02388; FemAB; 1.
SQ SEQUENCE 414 AA; 49110 MW; 336D9BA80541E260 CRC64;

Query Match 100.0%; Score 2176; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 4.9e-119;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKFSTLSBEEFTNYTKKHFKHYTQSIELYNRNKINHEAHIVGVKNDKNEVIAACLLTEA 60

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Db 121 IIKNYNNSVIVKMLGKIGYLHQGYTTGYSNKSQIRWISVLDLKDNDENQLLKEMEYQTRR 180

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Db 361 NFYGITGVFSNEADDFGVQQFKKGFNAHVEELIGDFIKPVRPILYKFAKLIYKV 414